

GG	GCG	CGA	GCG	CCT	CAG	CGC	GGC	CGC	TCG	CTC	TCC	CCC	38
	Ala	Arg	Ala	Pro	Gln	Arg	Gly	Arg	Ser	Leu	Ser	Pro	
	1				5					10			
TCG	AGG	GAC	AAA	CTT	TTC	CCA	AAC	CCG	ATC	CGA	GCC	CTT	77
Ser	Arg	Asp	Lys	Leu	Phe	Pro	Asn	Pro	Ile	Arg	Ala	Leu	
		15					20					25	
GGA	CCA	AAC	TCG	CCT	GCG	CCG	AGA	GCC	GTC	CGC	GTA	GAG	116
Gly	Pro	Asn	Ser	Pro	Ala	Pro	Arg	Ala	Val	Arg	Val	Glu	
				30					35				
CGC	TCC	GTC	TCC	GGC	GAG	ATG	TCC	GAG	CGC	AAA	GAA	GGC	155
Arg	Ser	Val	Ser	Gly	Glu	Met	Ser	Glu	Arg	Lys	Glu	Gly	
	40					45					50		
AGA	GCG	AAA	GGG	AAG	GGC	AAG	AAG	AAG	GAG	CGA	GGC	TCC	194
Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Glu	Arg	Gly	Ser	
			55					60					
GGC	AAG	AAG	CCG	GAG	TCC	GCG	GCG	GGC	AGC	CAG	AGC	CCA	233
Gly	Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser	Pro	
	65				70					75			
GCC	TTG	CCT	CCC	CGA	TTG	AAA	GAG	ATG	AAA	AGC	CAG	GAA	272
Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	
		80					85					90	
TCG	GCT	GCA	GGT	TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	311
Ser	Ala	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	
				95					100				
AGT	TCT	GAA	TAC	TCC	TCT	CTC	AGA	TTC	AAG	TGG	TTC	AAG	350
Ser	Ser	Glu	Tyr	Ser	Ser	Leu	Arg	Phe	Lys	Trp	Phe	Lys	
	105					110					115		
AAT	GGG	AAT	GAA	TTG	AAT	CGA	AAA	AAC	AAA	CCA	CAA	AAT	389
Asn	Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys	Pro	Gln	Asn	
			120					125					
ATC	AAG	ATA	CAA	AAA	AAG	CCA	GGG	AAG	TCA	GAA	CTT	CGC	428
Ile	Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	Arg	
					135					140			
ATT	AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA	GAG	TAT	ATG	467
Ile	Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	
		145					150					155	
TGC	AAA	GTG	ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT	506
Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	
				160					165				

FIG. 1A

GCC	AAT	ATC	ACC	ATC	GTG	GAA	TCA	AAC	GAG	ATC	ATC	ACT	545
Ala	Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	Glu	Ile	Ile	Thr	
	170					175					180		
GGT	ATG	CCA	GCC	TCA	ACT	GAA	GGA	GCA	TAT	GTG	TCT	TCA	584
Gly	Met	Pro	Ala	Ser	Thr	Glu	Gly	Ala	Tyr	Val	Ser	Ser	
			185					190					
GAG	TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCC	ACA	GAA	GGA	GCA	623
Glu	Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	Gly	Ala	
195					200					205			
AAT	ACT	TCT	TCA	TCT	ACA	TCT	ACA	TCC	ACC	ACT	GGG	ACA	662
Asn	Thr	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Gly	Thr	
		210				215						220	
AGC	CAT	CTT	GTA	AAA	TGT	GCG	GAG	AAG	GAG	AAA	ACT	TTC	701
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	
				225					230				
TGT	GTG	AAT	GGA	GGG	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	740
Cys	Val	Asn	Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	
	235					240					245		
TCA	AAC	CCC	TCG	AGA	TAC	TTG	TGC	AAG	TGC	CAA	CCT	GGA	779
Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	Gln	Pro	Gly	
			250					255					
TTC	ACT	GGA	GCA	AGA	TGT	ACT	GAG	AAT	GTG	CCC	ATG	AAA	818
Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	Val	Pro	Met	Lys	
260					265					270			
GTC	CAA	AAC	CAA	GAA	AAG	GCG	GAG	GAG	CTG	TAC	CAG	AAG	857
Val	Gln	Asn	Gln	Glu	Lys	Ala	Glu	Glu	Leu	Tyr	Gln	Lys	
		275					280					285	
AGA	GTG	CTG	ACC	ATA	ACC	GGC	ATC	TGC	ATC	GCC	CTC	CTT	896
Arg	Val	Leu	Thr	Ile	Thr	Gly	Ile	Cys	Ile	Ala	Leu	Leu	
				290					295				
GTG	GTC	GGC	ATC	ATG	TGT	GTG	GTG	GCC	TAC	TGC	AAA	ACC	935
Val	Val	Gly	Ile	Met	Cys	Val	Val	Ala	Tyr	Cys	Lys	Thr	
	300					305					310		
AAG	AAA	CAG	CGG	AAA	AAG	CTG	CAT	GAC	CGT	CTT	CGG	CAG	974
Lys	Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	Arg	Leu	Arg	Gln	
			315					320					
AGC	CTT	CGG	TCT	GAA	CGA	AAC	AAT	ATG	ATG	AAC	ATT	GCC	1013
Ser	Leu	Arg	Ser	Glu	Arg	Asn	Asn	Met	Met	Asn	Ile	Ala	
325					330					335			

FIG. 1B

AAT	GGG	CCT	CAC	CAT	CCT	AAC	CCA	CCC	CCC	GAG	AAT	GTC	1052
Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	Pro	Glu	Asn	Val	
		340					345					350	
CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	AAC	GTC	ATC	TCC	1091
Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	Asn	Val	Ile	Ser	
				355					360				
AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG	ACA	TCC	TTT	1130
Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	Thr	Ser	Phe	
	365					370					375		
TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	CAT	CAC	TCC	ACT	1169
Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	His	Ser	Thr	
			380					385					
ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	TGG	AGC	AAC	GGA	1208
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	
					395					400			
CAC	ACT	GAA	AGC	ATC	CTT	TCC	GAA	AGC	CAC	TCT	GTA	ATC	1247
His	Thr	Glu	Ser	Ile	Leu	Ser	Glu	Ser	His	Ser	Val	Ile	
		405					410					415	
GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	CAC	AGC	AGC	CCA	1286
Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	His	Ser	Ser	Pro	
				420					425				
ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	GGC	ACA	GGA	GGC	1325
Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	Gly	Thr	Gly	Gly	
	430					435					440		
CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	GAA	1364
Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	Glu	
			445					450					
ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	GAA	AGG	1403
Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser	Glu	Arg	
					460					465			
TAT	GTG	TCA	GCC	ATG	ACC	ACC	CCG	GCT	CGT	ATG	TCA	CCT	1442
Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	
		470					475					480	
GTA	GAT	TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAA	TCG	CCC	CCT	1481
Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	
				485					490				
TCG	GAA	ATG	TCT	CCA	CCC	GTG	TCC	AGC	ATG	ACG	GTG	TCC	1520
Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	Met	Thr	Val	Ser	
	495					500					505		

FIG. 1C

ATG Met	CCT Pro	TCC Ser	ATG Met 510	GCG Ala	GTC Val	AGC Ser	CCC Pro	TTC Phe 515	ATG Met	GAA Glu	GAA Glu	GAG Glu	1559
AGA Arg 520	CCT Pro	CTA Leu	CTT Leu	CTC Leu	GTG Val 525	ACA Thr	CCA Pro	CCA Pro	AGG Arg	CTG Leu 530	CGG Arg	GAG Glu	1598
AAG Lys	AAG Lys	TTT Phe 535	GAC Asp	CAT His	CAC His	CCT Pro	CAG Gln 540	CAG Gln	TTC Phe	AGC Ser	TCC Ser	TTC Phe 545	1637
CAC His	CAC His	AAC Asn	CCC Pro	GCG Ala 550	CAT His	GAC Asp	AGT Ser	AAC Asn	AGC Ser 555	CTC Leu	CCT Pro	GCT Ala	1676
AGC Ser 560	CCC Pro	TTG Leu	AGG Arg	ATA Ile	GTG Val	GAG Glu 565	GAT Asp	GAG Glu	GAG Glu	TAT Tyr	GAA Glu 570	ACG Thr	1715
ACC Thr	CAA Gln	GAG Glu	TAC Tyr 575	GAG Glu	CCA Pro	GCC Ala	CAA Gln	GAG Glu 580	CCT Pro	GTT Val	AAG Lys	AAA Lys	1754
CTC Leu 585	GCC Ala	AAT Asn	AGC Ser	CGG Arg	CGG Arg 590	GCC Ala	AAA Lys	AGA Arg	ACC Thr	AAG Lys 595	CCC Pro	AAT Asn	1793
GGC Gly	CAC His	ATT Ile 600	GCT Ala	AAC Asn	AGA Arg	TTG Leu	GAA Glu 605	GTG Val	GAC Asp	AGC Ser	AAC Asn	ACA Thr 610	1832
AGC Ser	TCC Ser	CAG Gln	AGC Ser	AGT Ser 615	AAC Asn	TCA Ser	GAG Glu	AGT Ser	GAA Glu 620	ACA Thr	GAA Glu	GAT Asp	1871
GAA Glu 625	AGA Arg	GTA Val	GGT Gly	GAA Glu	GAT Asp	ACG Thr 630	CCT Pro	TTC Phe	CTG Leu	GGC Gly	ATA Ile 635	CAG Gln	1910
AAC Asn	CCC Pro	CTG Leu	GCA Ala 640	GCC Ala	AGT Ser	CTT Leu	GAG Glu	GCA Ala 645	ACA Thr	CCT Pro	GCC Ala	TTC Phe	1949
CGC Arg 650	CTG Leu	GCT Ala	GAC Asp	AGC Ser	AGG Arg 655	ACT Thr	AAC Asn	CCA Pro	GCA Ala	GGC Gly 660	CGC Arg	TTC Phe	1988
TCG Ser	ACA Thr	CAG Gln 665	GAA Glu	GAA Glu	ATC Ile	CAG Gln 669	G	2010					

FIG. 1D

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GG	GAC	AAA	CTT	TTC	CCA	AAC	CCG	ATC	CGA	GCC	CTT	GGA	38
	Asp	Lys	Leu	Phe	Pro	Asn	Pro	Ile	Arg	Ala	Leu	Gly	
	1				5					10			
CCA	AAC	TCG	CCT	GCG	CCG	AGA	GCC	GTC	CGC	GTA	GAG	CGC	77
Pro	Asn	Ser	Pro	Ala	Pro	Arg	Ala	Val	Arg	Val	Glu	Arg	
		15					20					25	
TCC	GTC	TCC	GGC	GAG	ATG	TCC	GAG	CGC	AAA	GAA	GGC	AGA	116
Ser	Val	Ser	Gly	Glu	Met	Ser	Glu	Arg	Lys	Glu	Gly	Arg	
				30					35				
GGC	AAA	GGG	AAG	GGC	AAG	AAG	AAG	GAG	CGA	GGC	TCC	GGC	155
Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Glu	Arg	Gly	Ser	Gly	
	40					45					50		
AAG	AAG	CCG	GAG	TCC	GCG	GCG	GGC	AGC	CAG	AGC	CCA	GCC	194
Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser	Pro	Ala	
			55					60					
TTG	CCT	CCC	CAA	TTG	AAA	GAG	ATG	AAA	AGC	CAG	GAA	TCG	233
Leu	Pro	Pro	Gln	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	
	65				70					75			
GCT	GCA	GGT	TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	AGT	272
Ala	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	
		80					85					90	
TCT	GAA	TAC	TCC	TCT	CTC	AGA	TTC	AAG	TGG	TTC	AAG	AAT	311
Ser	Glu	Tyr	Ser	Ser	Leu	Arg	Phe	Lys	Trp	Phe	Lys	Asn	
				95					100				
GGG	AAT	GAA	TTG	AAT	CGA	AAA	AAC	AAA	CCA	CAA	AAT	ATC	350
Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys	Pro	Gln	Asn	Ile	
	105					110					115		
AAG	ATA	CAA	AAA	AAG	CCA	GGG	AAG	TCA	GAA	CTT	CGC	ATT	389
Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	Arg	Ile	
			120					125					
AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA	GAG	TAT	ATG	TGC	428
Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	Cys	
					135					140			
AAA	GTG	ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	467
Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	
		145					150					155	
AAT	ATC	ACC	ATC	GTG	GAA	TCA	AAC	GAG	ATC	ATC	ACT	GGT	506
Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	Glu	Ile	Ile	Thr	Gly	
				160					165				

FIG. 2A

ATG	CCA	GCC	TCA	ACT	GAA	GGA	GCA	TAT	GTG	TCT	TCA	GAG	545
Met	Pro	Ala	Ser	Thr	Glu	Gly	Ala	Tyr	Val	Ser	Ser	Glu	
	170					175						180	
TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCC	ACA	GAA	GGA	GCA	AAT	584
Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	Gly	Ala	Asn	
			185					190					
ACT	TCT	TCA	TCT	ACA	TCT	ACA	TCC	ACC	ACT	GGG	ACA	AGC	623
Thr	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Gly	Thr	Ser	
195					200					205			
CAT	CTT	GTA	AAA	TGT	GCG	GAG	AAG	GAG	AAA	ACT	TTC	TGT	662
His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	
		210					215					220	
GTG	AAT	GGA	GGG	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	701
Val	Asn	Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	
				225					230				
AAC	CCC	TCG	AGA	TAC	TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	740
Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	
	235					240					245		
ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	GCC	AGC	TTC	779
Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Phe	
			250					255					
TAC	AAG	CAT	CTT	GGG	ATT	GAA	TTT	ATG	GAG	GCG	GAG	GAG	818
Tyr	Lys	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ala	Glu	Glu	
260					265					270			
CTG	TAC	CAG	AAG	AGA	GTG	CTG	ACC	ATA	ACC	GGC	ATC	TGC	857
Leu	Tyr	Gln	Lys	Arg	Val	Leu	Thr	Ile	Thr	Gly	Ile	Cys	
		275					280					285	
ATC	GCC	CTC	CTT	GTG	GTC	GGC	ATC	ATG	TGT	GTG	GTG	GCC	896
Ile	Ala	Leu	Leu	Val	Val	Gly	Ile	Met	Cys	Val	Val	Ala	
				290					295				
TAC	TGC	AAA	ACC	AAG	AAA	CAG	CGG	AAA	AAG	CTG	CAT	GAC	935
Tyr	Cys	Lys	Thr	Lys	Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	
	300					305					310		
CGT	CTT	CGG	CAG	AGC	CTT	CGG	TCT	GAA	CGA	AAC	AAT	ATG	974
Arg	Leu	Arg	Gln	Ser	Leu	Arg	Ser	Glu	Arg	Asn	Asn	Met	
			315					320					
ATG	AAC	ATT	GCC	AAT	GGG	CCT	CAC	CAT	CCT	AAC	CCA	CCC	1013
Met	Asn	Ile	Ala	Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	
325					330					335			

FIG. 2B

CCC	GAG	AAT	GTC	CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	1052
Pro	Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	
		340					345					350	
AAC	GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	1091
Asn	Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	
				355					360				
GAG	ACA	TCC	TTT	TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	1130
Glu	Thr	Ser	Phe	Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	
	365					370					375		
CAT	CAC	TCC	ACT	ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	1169
His	His	Ser	Thr	Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	
			380					385					
TGG	AGC	AAC	GGA	CAC	ACT	GAA	AGC	ATC	CTT	TCC	GAA	AGC	1208
Trp	Ser	Asn	Gly	His	Thr	Glu	Ser	Ile	Leu	Ser	Glu	Ser	
	390				395					400			
CAC	TCT	GTA	ATC	GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	1247
His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	
		405					410					415	
CAC	AGC	AGC	CCA	ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	1286
His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	
				420					425				
GGC	ACA	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	1325
Gly	Thr	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	
	430					435					440		
CAT	GCC	AGA	GAA	ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	1364
His	Ala	Arg	Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	
			445					450					
CAT	AGT	GAA	AGG	TAT	GTG	TCA	GCC	ATG	ACC	ACC	CCG	GCT	1403
His	Ser	Glu	Arg	Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	
	455				460					465			
CGT	ATG	TCA	CCT	GTA	GAT	TTC	CAC	ACG	CCA	AGC	TCC	CCC	1442
Arg	Met	Ser	Pro	Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	
		470					475					480	
AAA	TCG	CCC	CCT	TCG	GAA	ATG	TCT	CCA	CCC	GTG	TCC	AGC	1481
Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	
				485					490				
ATG	ACG	GTG	TCC	ATG	CCT	TCC	ATG	GCG	GTC	AGC	CCC	TTC	1520
Met	Thr	Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro	Phe	
	495					500					505		

FIG. 2C

GAC AGC AAC ACA AGC TCC CAG AGC AGT AAC TCA GAG AGT 1832
Asp Ser Asn Thr Ser Ser Ser Gln Ser Ser Asn Ser Glu Ser 610
600 605

FIG. 2D


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GAA ACA GAA GAT GAA AGA GTA GGT GAA GAT ACG CCT TTC 1871
Glu Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe
615 620

CTG GGC ATA CAG AAC CCC CTG GCA GCC AGT CTT GAG GCA 1910
Leu Gly Ile Gln Asn Pro Leu Ala Ala Ser Leu Glu Ala
625 630 635

ACA CCT GCC TTC CGC CTG GCT GAC AGC AGG ACT AAC CCA 1949
Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg Thr Asn Pro
640 645

GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC CAG GCC AGG 1988
Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln Ala Arg
650 655 660

CTG TCT AGT GTA ATT GCT AAC CAA GAC CCT ATT GCT GTA TA 2029
Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val
665 670 675

A AACCTAAATA AACACATAGA TTCACCTGTA AACCTTTATT 2070

TTATATAATA AAGTATTCCA CCTTAAATTA AACAAATTAT TTTATTTTAG 2120

CAGTTCTGCA AATAGAAAAC AGGAAAAAAA CTTTATATAAA TTAAATATAT 2170

GTATGTAAAA ATGAAAAAAA AAAAAAAA 2199

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FIG. 2E

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GTGGCTGCGG GGCAATTGAA AAAGAGCCGG CGAGGAGTTC CCCGAAACTT 50

GTTGGAAGTC CGGGCTCGCG CGGAGGCCAG GAGCTGAGCG GCGGCGGCTG 100

CCGGACGATG GGAGCGTGAG CAGGACGGTG ATAACCTCTC CCCGATCGGG 150

TTGCGAGGGC GCCGGGCAGA GGCCAGGACG CGAGCCGCCA GCGGCGGGAC 200

CCATCGACGA CTTCCCGGGG CGACAGGAGC AGCCCCGAGA GCCAGGGCGA 250

GCGCCCGTTC CAGGTGGCCG GACCGCCCGC CGCGTCCGCG CCGCGCTCCC 300

TGCAGGCAAC GGGAGACGCC CCCGCGCAGC GCGAGCGCCT CAGCGCGGCC 350

GCTCGCTCTC CCCATCGAGG GACAACTTT TCCCAAACCC GATCCGAGCC 400

CTTGGACCAA ACTCGCCTGC GCCGAGAGCC GTCCGCGTAG AGCGCTCCGT 450

CTCCGGCGAG ATG TCC GAG CGC AAA GAA GGC AGA GGC AAA 490
Met Ser Glu Arg Lys Glu Gly Arg Gly Lys
1 5 10

GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC AAG AAG 529
Gly Lys Gly Lys Lys Lys Glu Arg Gly Ser Gly Lys Lys
15 20

CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA GCC TTG CCT 568
Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro
25 30 35

CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA 607
Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala
40 45

GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA 646
Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
50 55 60

TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG AAT GGG AAT 685
Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn
65 70 75

GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT ATC AAG ATA 724
Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile
80 85

FIG. 3A

FIG. 3B

CTG	CAT	GAC	CGT	CTT	CGG	CAG	AGC	CTT	CGG	TCT	GAA	CGA	1309
Leu	His	Asp	Arg	Leu	Arg	Gln	Ser	Leu	Arg	Ser	Glu	Arg	
				275						280			
AAC	AAT	ATG	ATG	AAC	ATT	GCC	AAT	GGG	CCT	CAC	CAT	CCT	1348
Asn	Asn	Met	Met	Asn	Ile	Ala	Asn	Gly	Pro	His	His	Pro	
	285					290					295		
AAC	CCA	CCC	CCC	GAG	AAT	GTC	CAG	CTG	GTG	AAT	CAA	TAC	1387
Asn	Pro	Pro	Pro	Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	
			300					305					
GTA	TCT	AAA	AAC	GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	1426
Val	Ser	Lys	Asn	Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	
310					315					320			
AGA	GAA	GCA	GAG	ACA	TCC	TTT	TCC	ACC	AGT	CAC	TAT	ACT	1465
Arg	Glu	Ala	Glu	Thr	Ser	Phe	Ser	Thr	Ser	His	Tyr	Thr	
		325					330					335	
TCC	ACA	GCC	CAT	CAC	TCC	ACT	ACT	GTC	ACC	CAG	ACT	CCT	1504
Ser	Thr	Ala	His	His	Ser	Thr	Thr	Val	Thr	Gln	Thr	Pro	
				340						345			
AGC	CAC	AGC	TGG	AGC	AAC	GGA	CAC	ACT	GAA	AGC	ATC	CTT	1543
Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu	Ser	Ile	Leu	
	350					355					360		
TCC	GAA	AGC	CAC	TCT	GTA	ATC	GTG	ATG	TCA	TCC	GTA	GAA	1582
Ser	Glu	Ser	His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	
			365					370					
AAC	AGT	AGG	CAC	AGC	AGC	CCA	ACT	GGG	GGC	CCA	AGA	GGA	1621
Asn	Ser	Arg	His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	
375					380					385			
CGT	CTT	AAT	GGC	ACA	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	1660
Arg	Leu	Asn	Gly	Thr	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	
		390					395					400	
TTC	CTC	AGG	CAT	GCC	AGA	GAA	ACC	CCT	GAT	TCC	TAC	CGA	1699
Phe	Leu	Arg	His	Ala	Arg	Glu	Thr	Pro	Asp	Ser	Tyr	Arg	
				405					410				
GAC	TCT	CCT	CAT	AGT	GAA	AGG	TAT	GTG	TCA	GCC	ATG	ACC	1738
Asp	Ser	Pro	His	Ser	Glu	Arg	Tyr	Val	Ser	Ala	Met	Thr	
	415					420					425		
ACC	CCG	GCT	CGT	ATG	TCA	CCT	GTA	GAT	TTC	CAC	ACG	CCA	1777
Thr	Pro	Ala	Arg	Met	Ser	Pro	Val	Asp	Phe	His	Thr	Pro	
			430					435					
AGC	TCC	CCC	AAA	TCG	CCC	CCT	TCG	GAA	ATG	TCT	CCA	CCC	1816
Ser	Ser	Pro	Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro	Pro	
440					445					450			

FIG. 3C

GTG	TCC	AGC	ATG	ACG	GTG	TCC	AAG	CCT	TCC	ATG	GCG	GTC	1855
Val	Ser	Ser	Met	Thr	Val	Ser	Lys	Pro	Ser	Met	Ala	Val	
		455					460					465	
AGC	CCC	TTC	ATG	GAA	GAA	GAG	AGA	CCT	CTA	CTT	CTC	GTG	1894
Ser	Pro	Phe	Met	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	
				470					475				
ACA	CCA	CCA	AGG	CTG	CGG	GAG	AAG	AAG	TTT	GAC	CAT	CAC	1933
Thr	Pro	Pro	Arg	Leu	Arg	Glu	Lys	Lys	Phe	Asp	His	His	
	480					485					490		
CCT	CAG	CAG	TTC	AGC	TCC	TTC	CAC	CAC	AAC	CCC	GCG	CAT	1972
Pro	Gln	Gln	Phe	Ser	Ser	Phe	His	His	Asn	Pro	Ala	His	
			495					500					
GAC	AGT	AAC	AGC	CTC	CCT	GCT	AGC	CCC	TTG	AGG	ATA	GTG	2011
Asp	Ser	Asn	Ser	Leu	Pro	Ala	Ser	Pro	Leu	Arg	Ile	Val	
505					510					515			
GAG	GAT	GAG	GAG	TAT	GAA	ACG	ACC	CAA	GAG	TAC	GAG	CCA	2050
Glu	Asp	Glu	Glu	Tyr	Glu	Thr	Thr	Gln	Glu	Tyr	Glu	Pro	
		520					525					530	
GCC	CAA	GAG	CCT	GTT	AAG	AAA	CTC	GCC	AAT	AGC	CGG	CGG	2089
Ala	Gln	Glu	Pro	Val	Lys	Lys	Leu	Ala	Asn	Ser	Arg	Arg	
				535					540				
GCC	AAA	AGA	ACC	AAG	CCC	AAT	GGC	CAC	ATT	GCT	AAC	AGA	2128
Ala	Lys	Arg	Thr	Lys	Pro	Asn	Gly	His	Ile	Ala	Asn	Arg	
	545					550					555		
TTG	GAA	GTG	GAC	AGC	AAC	ACA	AGC	TCC	CAG	AGC	AGT	AAC	2167
Leu	Glu	Val	Asp	Ser	Asn	Thr	Ser	Ser	Gln	Ser	Ser	Asn	
			560					565					
TCA	GAG	AGT	GAA	ACA	GAA	GAT	GAA	AGA	GTA	GGT	GAA	GAT	2206
Ser	Glu	Ser	Glu	Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	
570					575					580			
ACG	CCT	TTC	CTG	GGC	ATA	CAG	AAC	CCC	CTG	GCA	GCC	AGT	2245
Thr	Pro	Phe	Leu	Gly	Ile	Gln	Asn	Pro	Leu	Ala	Ala	Ser	
		585					590					595	
CTT	GAG	GCA	ACA	CCT	GCC	TTC	CGC	CTG	GCT	GAC	AGC	AGG	2284
Leu	Glu	Ala	Thr	Pro	Ala	Phe	Arg	Leu	Ala	Asp	Ser	Arg	
				600					605				
ACT	AAC	CCA	GCA	GGC	CGC	TTC	TCG	ACA	CAG	GAA	GAA	ATC	2323
Thr	Asn	Pro	Ala	Gly	Arg	Phe	Ser	Thr	Gln	Glu	Glu	Ile	
	610					615					620		
CAG	GCC	AGG	CTG	TCT	AGT	GTA	ATT	GCT	AAC	CAA	GAC	CCT	2362
Gln	Ala	Arg	Leu	Ser	Ser	Val	Ile	Ala	Asn	Gln	Asp	Pro	
			625					630					

FIG. 3D

ATT GCT GTA TAAACCTA AATAACACA TAGATTCACC TGTAACACTT 2410
 Ile Ala Val
 635 637

TATTTTATAT AATAAGTAT TCCACCTTAA ATTAAACAAT TTATTTTATT 2460

TTAGCAGTTC TGCAAATAAA AAAAAAAAAA 2490

FIG. 3E

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GCGCCTGCCT CCAACCTGCG GCGGGAGGT GGGTGGCTGC GGGGCAATTG 50
 AAAAAGAGCC GCGAGGAGT TCCCCGAAAC TTGTTGGAAC TCCGGGCTCG 100
 CGCGGAGGCC AGGAGCTGAG CGGCGGCGGC TGCCGGACGA TGGGAGCGTG 150
 AGCAGGACGG TGATAACCTC TCCCCGATCG GGTTCGAGG GCGCCGGGCA 200
 GAGGCCAGGA CGCGAGCCGC CAGCGGCGGG ACCCATCGAC GACTTCCCGG 250
 GGCGACAGGA GCAGCCCCGA GAGCCAGGGC GAGCGCCCGT TCCAGGTGGC 300
 CGGACCGCCC GCCGCGTCCG CGCCGCGCTC CCTGCAGGCA ACGGGAGACG 350
 CCCCCGCGCA GCGCGAGCGC CTCAGCGCGG CCGCTCGCTC TCCCCATCGA 400
 GGGACAAACT TTTCCCAAAC CCGATCCGAG CCCTTGGACC AAACTCGCCT 450
 GCGCCGAGAG CCGTCCGCGT AGAGCGCTCC GTCTCCGGCG AG ATG 495
 Met
 1
 TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 534
 Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys
 5 10
 AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 573
 Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala
 15 20 25
 GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 612
 Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys
 30 35 40
 GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 651
 Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
 45 50
 GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 690
 Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
 55 60 65
 AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 729
 Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg
 70 75

FIG. 4A

AAA	AAC	AAA	CCA	CAA	AAT	ATC	AAG	ATA	CAA	AAA	AAG	CCA	768
Lys	Asn	Lys	Pro	Gln	Asn	Ile	Lys	Ile	Gln	Lys	Lys	Pro	
80					85					90			
GGG	AAG	TCA	GAA	CTT	CGC	ATT	AAC	AAA	GCA	TCA	CTG	GCT	807
Gly	Lys	Ser	Glu	Leu	Arg	Ile	Asn	Lys	Ala	Ser	Leu	Ala	
		95					100					105	
GAT	TCT	GGA	GAG	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	TTA	846
Asp	Ser	Gly	Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	
				110						115			
GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAT	ATC	ACC	ATC	GTG	GAA	885
Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	Ile	Thr	Ile	Val	Glu	
	120					125					130		
TCA	AAC	GAG	ATC	ATC	ACT	GGT	ATG	CCA	GCC	TCA	ACT	GAA	924
Ser	Asn	Glu	Ile	Ile	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu	
			135					140					
GGA	GCA	TAT	GTG	TCT	TCA	GAG	TCT	CCC	ATT	AGA	ATA	TCA	963
Gly	Ala	Tyr	Val	Ser	Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	
145					150					155			
GTA	TCC	ACA	GAA	GGA	GCA	AAT	ACT	TCT	TCA	TCT	ACA	TCT	1002
Val	Ser	Thr	Glu	Gly	Ala	Asn	Thr	Ser	Ser	Ser	Thr	Ser	
		160					165					170	
ACA	TCC	ACC	ACT	GGG	ACA	AGC	CAT	CTT	GTA	AAA	TGT	GCG	1041
Thr	Ser	Thr	Thr	Gly	Thr	Ser	His	Leu	Val	Lys	Cys	Ala	
				175					180				
GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGG	GAG	TGC	1080
Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	
	185					190					195		
TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAC	CCC	TCG	AGA	TAC	TTG	1119
Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	
			200					205					
TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	1158
Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	
210					215					220			
AAC	TAC	GTA	ATG	GCC	AGC	TTC	TAC	AGT	ACG	TCC	ACT	CCC	1197
Asn	Tyr	Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	Thr	Pro	
		225					230					235	
TTT	CTG	TCT	CTG	CCT	GAA	TAGGA	GCATGCTCAG	TTGGTGCTGC					1240
Phe	Leu	Ser	Leu	Pro	Glu								
				240	241								
TTTCTTGTTG	CTGCATCTCC	CCTCAGATTC	CACCTAGAGC	TAGATGTGTC									1290

FIG. 4B

TTACCAGATC TAATATTGAC TGCCTCTGCC TGTCGCATGA GAACATTAAC 1340
AAAAGCAATT GTATTACTTC CTCTGTTCGC GACTAGTTGG CTCTGAGATA 1390
CTAATAGGTG TGTGAGGCTC CGGATGTTTC TGGAATTGAT ATTGAATGAT 1440
GTGATACAAA TTGATAGTCA ATATCAAGCA GTGAAATATG ATAATAAAGG 1490
CATTTCAAAG TCTCACTTTT ATTGATAAAA TAAAAATCAT TCTACTGAAC 1540
AGTCCATCTT CTTTATACAA TGACCACATC CTGAAAAGGG TGTGCTAAG 1590
CTGTAACCGA TATGCACTTG AAATGATGGT AAGTTAATTT TGATTCAGAA 1640
TGTGTTATTT GTCACAAATA AACATAATAA AAGGAGTTCA GATGTTTTTC 1690
TTCATTAACC AAAAAAAAAA AAAAA 1715

FIG. 4C

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GAGGCGCCTG CCTCCAACCT GCGGGCGGGA GGTGGGTGGC TCGGGGGCAA 50

TTGAAAAAGA GCCGGCGAGG AGTTCCCCGA AACTTGTTGG AACTCCGGGC 100

TCGCGCGGAG GCCAGGAGCT GAGCGGCGGC GGCTGCCGGA CGATGGGAGC 150

GTGAGCAGGA CGGTGATAAC CTCTCCCCGA TCGGGTTGCG AGGCGGCCGG 200

GCAGAGGCCA GGACGCGAGC CGCCAGCGGC GGGACCCATC GACGACTTCC 250

CGGGGCGACA GGAGCAGCCC CGAGAGCCAG GGCAGCGCC CGTTCCAGGT 300

GGCCGGACCG CCCGCCGCGT CCGCGCCGCG CTCCTGCAG GCAACGGGAG 350

ACGCCCCCGC GCAGCGCGAG CGCCTCAGCG CGGCCGCTCG CTCTCCCCAT 400

CGAGGGACAA ACTTTTCCCA AACCCGATCC GAGCCCTTGG ACCAAACTCG 450

CCTGCGCCGA GAGCCGTCCG CGTAGAGCGC TCCGTCTCCG GCGAG AT 497
Met
1

G TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 537
Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys
5 10

AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 576
Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala
15 20 25

GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 615
Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys
30 35 40

GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 654
Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
45 50

GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 693
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
55 60 65

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 732
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg
70 75

FIG. 5A

AAA	AAC	AAA	CCA	CAA	AAT	ATC	AAG	ATA	CAA	AAA	AAG	CCA	771
Lys	Asn	Lys	Pro	Gln	Asn	Ile	Lys	Ile	Gln	Lys	Lys	Pro	
80					85					90			
GGG	AAG	TCA	GAA	CTT	CGC	ATT	AAC	AAA	GCA	TCA	CTG	GCT	810
Gly	Lys	Ser	Glu	Leu	Arg	Ile	Asn	Lys	Ala	Ser	Leu	Ala	
		95					100					105	
GAT	TCT	GGA	GAG	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	TTA	849
Asp	Ser	Gly	Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	
				110					115				
GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAT	ATC	ACC	ATC	GTG	GAA	888
Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	Ile	Thr	Ile	Val	Glu	
	120					125					130		
TCA	AAC	GAG	ATC	ATC	ACT	GGT	ATG	CCA	GCC	TCA	ACT	GAA	927
Ser	Asn	Glu	Ile	Ile	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu	
			135					140					
GGA	GCA	TAT	GTG	TCT	TCA	GAG	TCT	CCC	ATT	AGA	ATA	TCA	966
Gly	Ala	Tyr	Val	Ser	Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	
145					150					155			
GTA	TCC	ACA	GAA	GGA	GCA	AAT	ACT	TCT	TCA	TCT	ACA	TCT	1005
Val	Ser	Thr	Glu	Gly	Ala	Asn	Thr	Ser	Ser	Ser	Thr	Ser	
		160					165					170	
ACA	TCC	ACC	ACT	GGG	ACA	AGC	CAT	CTT	GTA	AAA	TGT	GCG	1044
Thr	Ser	Thr	Thr	Gly	Thr	Ser	His	Leu	Val	Lys	Cys	Ala	
				175					180				
GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGG	GAG	TGC	1083
Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	
	185					190					195		
TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAC	CCC	TCG	AGA	TAC	TTG	1122
Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	
			200					205					
TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	1161
Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	
210					215					220			
AAC	TAC	GTA	ATG	GCC	AGC	TTC	TAC	AAG	GCG	GAG	GAG	CTG	1200
Asn	Tyr	Val	Met	Ala	Ser	Phe	Tyr	Lys	Ala	Glu	Glu	Leu	
		225					230					235	
TAC	CAG	AAG	AGA	GTG	CTG	ACC	ATA	ACC	GGC	ATC	TGC	ATC	1239
Tyr	Gln	Lys	Arg	Val	Leu	Thr	Ile	Thr	Gly	Ile	Cys	Ile	
				240					245				
GCC	CTC	CTT	GTG	GTC	GGC	ATC	ATG	TGT	GTG	GTG	GCC	TAC	1278
Ala	Leu	Leu	Val	Val	Gly	Ile	Met	Cys	Val	Val	Ala	Tyr	
	250					255					260		

FIG. 5B

TGC	AAA	ACC	AAG	AAA	CAG	CGG	AAA	AAG	CTG	CAT	GAC	CGT	1317
Cys	Lys	Thr	Lys	Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	Arg	
			265					270					
CTT	CGG	CAG	AGC	CTT	CGG	TCT	GAA	CGA	AAC	AAT	ATG	ATG	1356
Leu	Arg	Gln	Ser	Leu	Arg	Ser	Glu	Arg	Asn	Asn	Met	Met	
275					280					285			
AAC	ATT	GCC	AAT	GGG	CCT	CAC	CAT	CCT	AAC	CCA	CCC	CCC	1395
Asn	Ile	Ala	Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	Pro	
		290					295					300	
GAG	AAT	GTC	CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	AAC	1434
Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	Asn	
				305					310				
GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG	1473
Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	
	315					320					325		
ACA	TCC	TTT	TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	CAT	1512
Thr	Ser	Phe	Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	
			330					335					
CAC	TCC	ACT	ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	TGG	1551
His	Ser	Thr	Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	
340					345					350			
AGC	AAC	GGA	CAC	ACT	GAA	AGC	ATC	CTT	TCC	GAA	AGC	CAC	1590
Ser	Asn	Gly	His	Thr	Glu	Ser	Ile	Leu	Ser	Glu	Ser	His	
		355				360						365	
TCT	GTA	ATC	GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	CAC	1629
Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	His	
				370					375				
AGC	AGC	CCA	ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	GGC	1668
Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	Gly	
	380					385					390		
ACA	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	1707
Thr	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	
			395					400					
GCC	AGA	GAA	ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	CAT	1746
Ala	Arg	Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	
405					410					415			
AGT	GAA	AGG	TAAAA	CCGAAGGCAA	AGCTACTGCA	GAGGAGAAAC	1790						
Ser	Glu	Arg											
		420											

TCAGTCAGAG AATCCCTGTG AGCACCTGCG GTCTCACCTC AGGAAATCTA 1840
CTCTAATCAG AATAAGGGGC GGCAGTTACC TGTCTAGGA GTGCTCCTAG 1890
TTGATGAAGT CATCTCTTTG TTTGACGGAA CTTATTTCTT CTGAGCTTCT 1940
CTCGTCGTCC CAGTGA CTGA CAGGCAACAG ACTCTTAAAG AGCTGGGATG 1990
CTTTGATGCG GAAGGTGCAG CACATGGAGT TTCCAGCTCT GCCATGGGC 2040
TCAGACCCAC TCGGGGTCTC AGTGTCTCA GTTGTAACAT TAGAGAGATG 2090
GCATCAATGC TTGATAAGGA CCCTTCTATA ATTCCAATTG CCAGTTATCC 2140
AAACTCTGAT TCGGTGGTCG AGCTGGCCTC GTGTTCTTAT CTGCTAACCC 2190
TGTCTTACCT TCCAGCCTCA GTTAAGTCAA ATCAAGGGCT ATGTCATTGC 2240
TGAATGTCAT GGGGGGCAAC TGCTTGCCCT CCACCCTATA GTATCTATTT 2290
TATGAAATTC CAAGAAGGGA TGAATAAATA AATCTCTTGG ATGCTGCGTC 2340
TGGCAGTCTT CACGGGTGGT TTTCAAAGCA GAAAAAAAAA AAAAAAAAAA 2390
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 2431

FIG. 5D

16	1	MSERKEGRGKGKGKKKERGS	GK	PP	RL	KEMKS	QES	AAG
11	1	MSERKEGRGKGKGKKKERGS	GK	PP	QL	KEMKS	QES	AAG
76	1	MSERKEGRGKGKGKKKERGS	GK	PP	QL	KEMKS	QES	AAG
84	1	MSERKEGRGKGKGKKKERGS	GK	PP	QL	KEMKS	QES	AAG
78	1	MSERKEGRGKGKGKKKERGS	GK	PP	QL	KEMKS	QES	AAG
16	51	SKLVLR	CET	SS	SE	YSS	SL	RF
11	51	SKLVLR	CET	SS	SE	YSS	SL	RF
76	51	SKLVLR	CET	SS	SE	YSS	SL	RF
84	51	SKLVLR	CET	SS	SE	YSS	SL	RF
78	51	SKLVLR	CET	SS	SE	YSS	SL	RF
16	101	KASL	AD	S	G	E	Y	M
11	101	KASL	AD	S	G	E	Y	M
76	101	KASL	AD	S	G	E	Y	M
84	101	KASL	AD	S	G	E	Y	M
78	101	KASL	AD	S	G	E	Y	M
16	151	ESPI	R	I	S	V	S	T
11	151	ESPI	R	I	S	V	S	T
76	151	ESPI	R	I	S	V	S	T
84	151	ESPI	R	I	S	V	S	T
78	151	ESPI	R	I	S	V	S	T

FIG. 6A

16	201	DLSNP	RYLCK	QPGFT	GARC	TEN	V	PMKV	QNQ	- - - -	EK	AEE	LYQ	KRV	LT
11	201	DLSNP	RYLCK	CPNE	FTG	DR	CQNY	V	MASF	YK	HLG	IE	FME	AEE	LYQ
76	201	DLSNP	RYLCK	CPNE	FTG	DR	CQNY	V	MASF	YK	- - - -	- - - -	- - - -	AEE	LYQ
84	201	DLSNP	RYLCK	CPNE	FTG	DR	CQNY	V	MASF	YK	- - - -	- - - -	- - - -	AEE	LYQ
78	201	DLSNP	RYLCK	CPNE	FTG	DR	CQNY	V	MASF	YK	- - - -	- - - -	- - - -	AEE	LYQ

16	246	ITGIC	IALL	VVG	IMCV	VAY	CKT	KKQ	RKKL	HDRL	RQSL	RSE	RNN	MMN	IANG
11	251	ITGIC	IALL	VVG	IMCV	VAY	CKT	KKQ	RKKL	HDRL	RQSL	RSE	RNN	MMN	IANG
76	243	ITGIC	IALL	VVG	IMCV	VAY	CKT	KKQ	RKKL	HDRL	RQSL	RSE	RNN	MMN	IANG
84	243	ITGIC	IALL	VVG	IMCV	VAY	CKT	KKQ	RKKL	HDRL	RQSL	RSE	RNN	MMN	IANG

16	296	PHHPN	PPPE	NVQL	VNQY	VSK	NV	ISSE	HIVER	EAE	TSF	STSH	YTS	TAH	HST
11	301	PHHPN	PPPE	NVQL	VNQY	VSK	NV	ISSE	HIVER	EAE	TSF	STSH	YTS	TAH	HST
76	293	PHHPN	PPPE	NVQL	VNQY	VSK	NV	ISSE	HIVER	EAE	TSF	STSH	YTS	TAH	HST
84	293	PHHPN	PPPE	NVQL	VNQY	VSK	NV	ISSE	HIVER	EAE	TSF	STSH	YTS	TAH	HST

16	346	TVTQT	PSHS	WSNG	HTES	ILSE	SHSV	IV	MSS	VENS	RHSS	P	TGG	PRG	RLNGT
11	351	TVTQT	PSHS	WSNG	HTES	ILSE	SHSV	IV	MSS	VENS	RHSS	P	TGG	PRG	RLNGT
76	343	TVTQT	PSHS	WSNG	HTES	ILSE	SHSV	IV	MSS	VENS	RHSS	P	TGG	PRG	RLNGT
84	343	TVTQT	PSHS	WSNG	HTES	ILSE	SHSV	IV	MSS	VENS	RHSS	P	TGG	PRG	RLNGT

FIG. 6B

16	396	GGPRECNSFLRHARETPD	SYRDS	PHSERYVS	AMTT	P	ARMSP	VD	FHT	PSSP
11	401	GGPRECNSFLRHARETPD	SYRDS	PHSERYVS	AMTT	P	ARMSP	VD	FHT	PSSP
76	393	GGPRECNSFLRHARETPD	SYRDS	PHSERYVS	AMTT	P	ARMSP	VD	FHT	PSSP
84	393	GGPRECNSFLRHARETPD	SYRDS	PHSER	-----					
16	446	KSPPSEMSPPVSSMTV	SMPSMA	VSPF	MEEER	PLLL	V	TP	PR	REKKFDHHP
11	451	KSPPSEMSPPVSSMTV	SMPSMA	VSPF	MEEER	PLLL	V	TP	PR	REKKFDHHP
76	443	KSPPSEMSPPVSSMTV	SMPSMA	VSPF	MEEER	PLLL	V	TP	PR	REKKFDHHP
16	496	QFSSFHHPAHDSNSL	PASPL	RIVED	EEYET	TQ	EYEP	AQ	EPV	KKLANSR
11	501	QFSSFHHPAHDSNSL	PASPL	RIVED	EEYET	TQ	EYEP	AQ	EPV	KKLANSR
76	493	QFSSFHHPAHDSNSL	PASPL	RIVED	EEYET	TQ	EYEP	AQ	EPV	KKLANSR
16	546	RAKRTKPNNGHIANR	LEVDS	NTSS	QSSNS	SESE	TE	DER	VGED	TPFLGIQNPL
11	551	RAKRTKPNNGHIANR	LEVDS	NTSS	QSSNS	SESE	TE	DER	VGED	TPFLGIQNPL
76	543	RAKRTKPNNGHIANR	LEVDS	NTSS	QSSNS	SESE	TE	DER	VGED	TPFLGIQNPL
16	596	AASLEATPAFRLAD	SRTNP	AGRF	STQ	EEI	Q	-----		
11	601	AASLEATPAFRLAD	SRTNP	AGRF	STQ	EEI	Q	ARL	SSV	IANQDPIAV
76	593	AASLEATPAFRLAD	SRTNP	AGRF	STQ	EEI	Q	ARL	SSV	IANQDPIAV

FIG. 6C

1 GGGTACCATGGGTTCGGTGAGCGCGTTTCCCGCCTGAGCGCAACTAGCGGC
 51 GGGTCGTGGGCACCTCCAGAAAAGATCCCGCACCATCCTCCAGGATCCAA
 101 TGGCCTTGGAGAGAGGGCTGCAGGGCCCCACGGACATTGCTGACTCTTCAG
 151 AACGTGCTGACATGGAGCCAGGTAGACTGAAATTATCATGTGTCCAAATT
 201 AAAATTGCATACTTCAAGGATTATTTGAAGGACTATTCTTAGACCCTTTT
 251 AAGAAGATTTAAAGAAAAACCACTCGGCCCTGAGTGCGGGCGAGGACCCTG

 301 TTTGTGGATGTGGAGGAGCGCGGGCCGGAGGCCATGGACGTGAAGGAGAG
 1 M D V K E R
 351 GAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGCCGCTACA
 7 K P Y R S L T R R R D A E R R Y T
 401 CCAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCGCAGAAATCGTAC
 24 S S S A D S E E G K A P Q K S Y
 451 AGCTCCAGCGAGACCCTGAAGGCCTACGACCAGGACGCCCGCCTAGCCTA
 40 S S S E T L K A Y D Q D A R L A Y
 501 TGGCAGCCGCGTCAAGGACATTGTGCCGACAGGAGGCCGAGGAATTCTGCC
 57 G S R V K D I V P Q E A E E F C R
 551 GCACAGGTGCCAACTTCACCCTGCGGGAGCTGGGGCTGGAAGAAGTAACG
 74 T G A N F T L R E L G L E E V T
 601 CCCCCTCACGGGACCCTGTACCGGACAGACATTGGCCTCCCCCACTGCGG
 90 P P H G T L Y R T D I G L P H C G
 651 CTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGC
 107 Y S M G A G S D A D M E A D T V L
 701 TGTCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGG
 124 S P E H P V R L W G R S T R S G
 751 CGCAGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGA
 140 R S S C L S S R A N S N L T L T D
 801 CACCGAGCATGAAAACACTGAGACTGATCATCCGGGGCGGCCTGCAGAACC
 157 T E H E N T E T D H P G G L Q N H
 851 ACGCGCGGCTCCGGACGCCGCGCCGCGCGCTCTCGCACGCCACACCCCC
 174 A R L R T P P P P L S H A H T P
 901 AACCAGCACCACGCGGCCTCCATTAACCTCCCTGAACCGGGGCAACTTCAC
 190 N Q H H A A S I N S L N R G N F T
 951 GCCGAGGAGCAACCCAGCCCCGGCCCCCACGGACCACTCGCTCTCCGGAG
 207 P R S N P S P A P T D H S L S G E
 1001 AGCCCCCTGCCGGCGGCGCCAGGAGCCTGCCACGCCAGGAGAACTGG
 224 P P A G G A Q E P A H A Q E N W
 1051 CTGCTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCC
 240 L L N S N I P L E T R N L G K Q P

FIG. 7A

2001 CACCACTGCCATTGCCTTGCCTCCCCGATTGAAAGAGATGAAAAGCCAGG
 557 T T A I A L P P R L K E M K S Q E
 2051 AATCGGCTGCAGGTTCCAAACTAGTCCTTCGGTGTGAAACCAGTTCTGAA
 574 S A A G S K L V L R C E T S S E
 2101 TACTCCTCTCTCAGATTCAAGTGGTTCAAGAATGGGAATGAATTGAATCG
 590 Y S S L R F K W F K N G N E L N R
 2151 AAAAAACAAACCACAAAATATCAAGATACAAAAAAGCCAGGGAAGTCAG
 607 K N K P Q N I K I Q K K P G K S E
 2201 AACTTCGCATTAAACAAAGCATCACTGGCTGATTCTGGAGAGTATATGTGC
 624 L R I N K A S L A D S G E Y M C
 2251 AAAGTGATCAGCAAATTAGGAAATGACAGTGCCTCTGCCAATATCACCAT
 640 K V I S K L G N D S A S A N I T I
 2301 CGTGGAATCAAACGAGATCATCACTGGTATGCCAGCCTCAACTGAAGGAG
 657 V E S N E I I T G M P A S T E G A
 2351 CATATGTGTCTTCAGAGTCTCCCATTAGAATATCAGTATCCACAGAAGGA
 674 Y V S S E S P I R I S V S T E G
 2401 GCAAATACTTCTTCATCTACATCTACATCCACCACTGGGACAAGCCATCT
 690 A N T S S S T S T S T T G T S H L
 2451 TGTAAATGTGCGGAGAAGGAGAAAACCTTTCTGTGTGAATGGAGGGGAGT
 707 V K (C) A E K E K T F (C) V N G G E (C)
 2501 GCTTCATGGTGAAGACCTTTCAAACCCCTCGAGATACTTGTGCAAGTGC
 724 F M V K D L S N P S R Y L (C) K (C)
 2551 CCAAATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGGCCAGCTT
 740 P N E F T G D R (C) Q N Y V M A S F
 2601 CTACAGTACGTCCACTCCCTTTCTGTCTCTGCCTGAATAGGAGCATGCTC
 757 Y S T S T P F L S L P E
 2651 AGTTGGTGCTGCTTTCTTGTTGCTGCATCTCCCCTCAGATTCCACCTAGA
 2701 GCTAGATGTGTCTTACCAGATCTAATATTGACTGCCTCTGCCTGTGCGCAT
 2751 GAGAACATTAACAAAAGCAATTGTATTACTTCCTCTGTTTCGCGACTAGTT
 2801 GGCTCTGAGATACTAATAGGTGTGTGAGGCTCCGGATGTTTCTGGAATTG
 2851 ATATTGAATGATGTGATACAAATTGATAGTCAATATCAAGCAGTGAAATA
 2901 TGATAATAAAGGCATTTCAAAGTCTCACTTTTATTGATAAAATAAAAATC
 2951 ATTCTACTGAACAGTCCATCTTCTTTATACAATGACCACATCCTGAAAAG
 3001 GGTGTTGCTAAGCTGTAACCGATATGCACTTGAAATGATGGTAAGTTAAT
 3051 TTTGATTCAGAATGTGTTATTTGTACAAATAAACATAATAAAAGGAAAA
 3101 AAAAAAAAAA

FIG. 7B

1101 ATTCCTAGGGACATTGCAGGACAACCTCATTGAGATGGACATTCTCGGCG
257 F L G T L Q D N L I E M D I L G A

1151 CCTCCCGCCATGATGGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCCT
274 S R H D G A Y S D G H F L F K P

1201 GGAGGCACCTCCCCGCTCTTCTGCACCACATCACCAGGGTACCCACTGAC
290 G G T S P L F C T T S P G Y P L T

1251 GTCCAGCACAGTGTACTCTCCTCCGCCCCGACCCCTGCCCCGCAGCACCT
307 S S T V Y S P P P R P L P R S T F

1301 TCGCCCGGCCCGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAAGTGG
324 A R P A F N L K K P S K Y C N W

1351 AAGTGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTTCATCCT
340 K C A A L S A I V I S A T L V I L

1401 GCTGGCATACTTTGTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGC
357 L A Y F V A M H L F G L N W H L Q

1451 AGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAGT
374 P M E G Q M Y E I T E D T A S S

1501 TGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGGCACTGGCTT
390 W P V P T D V S L Y P S G G T G L

1551 AGAGACCCCTGACAGGAAAGGCAAAGGAACACAGAAGGAAAGCCCAGTA
407 E T P D R K G K G T T E G K P S S

1601 GTTTCTTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGA
424 F F P E D S F I D S G E I D V G

1651 AGGCGAGCTTCCCAGAAGATTCCCTCCTGGCACTTTCTGGAGATCTCAAGT
440 R R A S Q K I P P G T F W R S Q V

1701 GTTCATAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGG
457 F I D H P V H L K F N V S L G K A

1751 CAGCCCTGGTTGGCATTATGAGCAGAAAAGGCCTCCCTCCTTCACATACA
474 A L V G I Y G R K G L P P S H T

1801 CAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCAGGA
490 Q F D F V E L L D G R R L L T Q E

1851 GGCGCGGAGCCTAGAGGGGACCCCGCGCCAGTCTCGGGGAACTGTGCCCC
507 A R S L E G T P R Q S R G T V P P

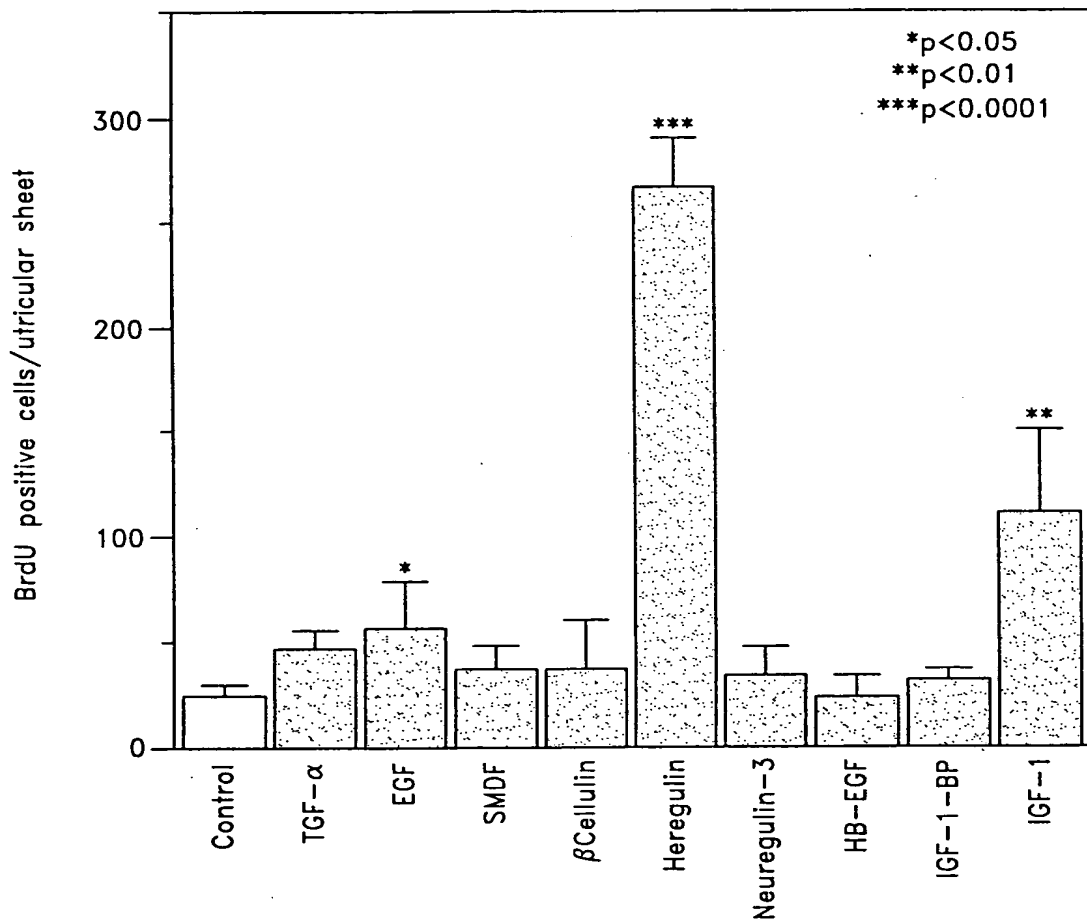
1901 CCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTTCAGGAATCTGG
524 S S H E T G F I Q Y L D S G I W

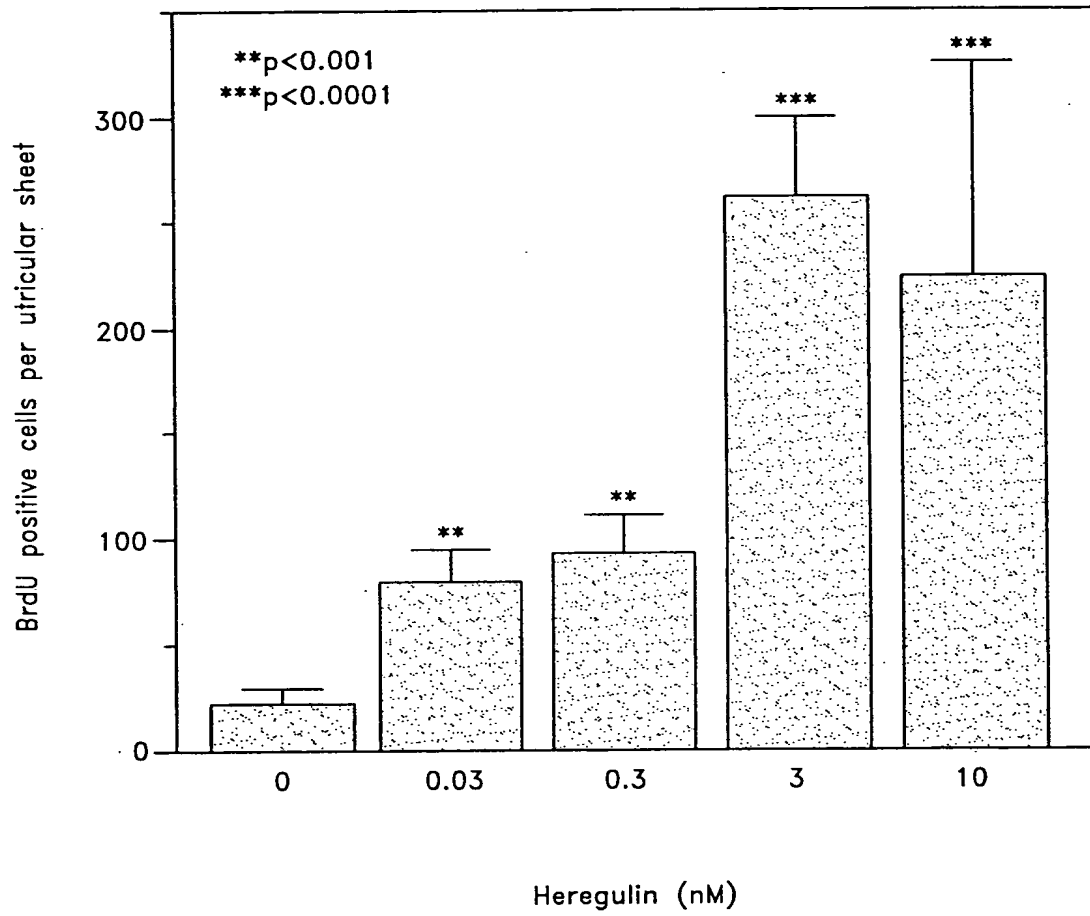
1951 CACTTGGCTTTTTTACAATGACGGAAAGGAGTCAGAAGTGGTTTCTTTCT
540 H L A F Y N D G K E S E V V S F L

1 GAATTCGGGACAGCCTCTCCTGCCGCGCTGCTGCTGCCGCCGCCGCCACCGCCGGCTGGTCTCTCTGCTTT
 76 TACTTCTCCTGCATGACAGTTGTTTTCTTTCATCTGAGCAGACACCAGCTTCAGATGCTCGAGGTGAGAAACATGC
 151 CTTTCAGTTTGGGCTACTGGTTTACTTAATTAATCAGCCGGCAGCTCCGTCGATCTATTTTCGTCCCTGTCTCT
 226 TGACGAGCCCGGGATGGTTTGGAGTAGCATTATAAAGAAGTAGAAAAGTGGCCAGAAAACAGCAGCTTAAAGAAT
 301 TATTACGATATACTTTGATTTTGTAGTTGCTAGGAGCTTTTCTTCCCCCTTGCATCTTTCTGAACTCTTCTTGA
 376 TTTTAATAATGGCCTTGGACTTGGACGATTTATCGATTTCCCCCTGTAAGATGCTGTATCATTTGGTTGGGGGG
 451 CCTCTGCGTGGTAATGGACCGTGAGAGCGGCCAGGCCTTCTTCTGGAGGTGAGCCGATGAGATTATTCCCCAG
 1 M E I Y S P D
 526 ACATGTCTGAGGTGCGCCGCCGAGAGGTCTCCAGCCCCCTCCACTCAGCTGAGTGCAGACCCATCTCTTGATGGGC
 8 M S E V A A E R S S S P S T Q L S A D P S L D G L
 601 TTCCGGCAGCAGAAGACATGCCAGAGCCCCAGACTGAAGATGGGAGAACCCCTGGACTCGTGGGCTGGCCGTGC
 33 P A A E D H P E P Q T E D G R T P G L V G L A V P
 676 CCTGCTGTGCGTGCCTAGAAGCTGAGCGCCTGAGAGGTTGCCTCAACTCAGAGAAAATCTGCATTGTCCCCATCC
 58 [C] [C] A [C] L E A E R L R G [C] L N S E K I [C] I V P I L
 751 TGGCTTGCCCTGGTCAGCCTCTGCCTCTGCATCGCCGGCCTCAAGTGGGTATTTGTGGACAAGATCTTTGAATATG
 83 A [C] L V S L [C] L [C] I A G L K W V F V D K I F E Y D
 826 ACTCTCTACTCACCTTGACCCTGGGGGTTAGGCCAGGACCCTATTATTTCTCTGGACGCAACTGCTGCCTCAG
 108 S P T H L D P G G L G Q D P I I S L D A T A A S A
 901 CTGTGTGGGTGTGCTCTGAGGCATACACTTCACCTGTCTCTAGGGCTCAATCTGAAAGTGAGGTTCAGTTACAG
 133 V W V S S E A Y T S P V S R A Q S E S E V Q V T V
 976 TGCAAGGTGACAAGGCTGTTGTCTCCTTTGAACCATCAGCGGCACCGACACCGAAGAATCGTATTTTGCCTTTT
 158 Q G D K A V V S F E P S A A P T P K N R I F A F S
 1051 CTTTCTTGCCG1CCACTGCGCCATCCTTCCCTTCACCCACCCGGAACCCCTGAGGTGAGAACGCCCAAGTCAGCAA
 183 F L P S T A P S F P S P T R N P E V R T P K S A T
 1126 CTCAGCCACAAACAACAGAACTAATCTCCAACTGCTCCTAACTTTCTACATCTACATCCACCACTGGGACAA
 208 Q P Q T T E T N L Q T A P K L S T S T S T T G T S
 1201 GCCATCTTGTAATAATGTGCGGAGAAGGAGAAAACCTTCTGTGTGAATGGAGGGGAGTGCTTCATGGTGAAAGACC
 233 H L V K [C] A E K E K T F [C] V N G G E [C] F M V K D L
 1276 TTTCAAACCCCTCGAGATACTTGTGCAAGTGCCAAATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGG
 258 S N P S R Y L [C] K [C] P N E F T G D R [C] Q N Y V M A
 1351 CCAGCTTCTACAGTACGTCCACTCCCTTTCTGTCTCTGCCTGAATAGGAGCATGCTCAGTTGGTGCTGCTTTCTT
 283 S F Y S T S T P F L S L P E O
 1426 GTTGCTGCATCTCCCTCAGATTCCACCTAGAGCTAGATGTGTCTTACCAGATCTAATATTGACTGCCTCTGCCT
 1501 GTCGATGAGAACATTAACAAAAGCAATTGTATTACTTCCTCTGTTGCGACTAGTTGGCTCTGAGATACTAATA
 1576 GGTGTGTGAGGCTCCGGATGTTTCTGGAATTGATATTGAATGATGTGATACAAATTGATAGTCAATATCAAGCAG
 1651 TGAAATATGATAATAAAGGCATTTCAAAGTCTCACTTTTATTGATAAAAATAAAATCATTCTACTGAACAGTCCA
 1726 TCTTCTTTATACAAATGACCACATCCTGAAAAGGGTGTGCTAAGCTGTAACCGATATGCACTTGAAATGATGGTA
 1801 AGTTAATTTTGATTTCAGAATGTGTTATTTGTACAAATAAACATAATAAAAGGAAAAAAAAAACCCGAATTC

EGF
-like

FIG. 8

*FIG. 9*

*FIG. 10*

Heregulin increases the number of 3H-thymidine labeled cells in supporting and hair cell layers in gentamicin-treated utricles

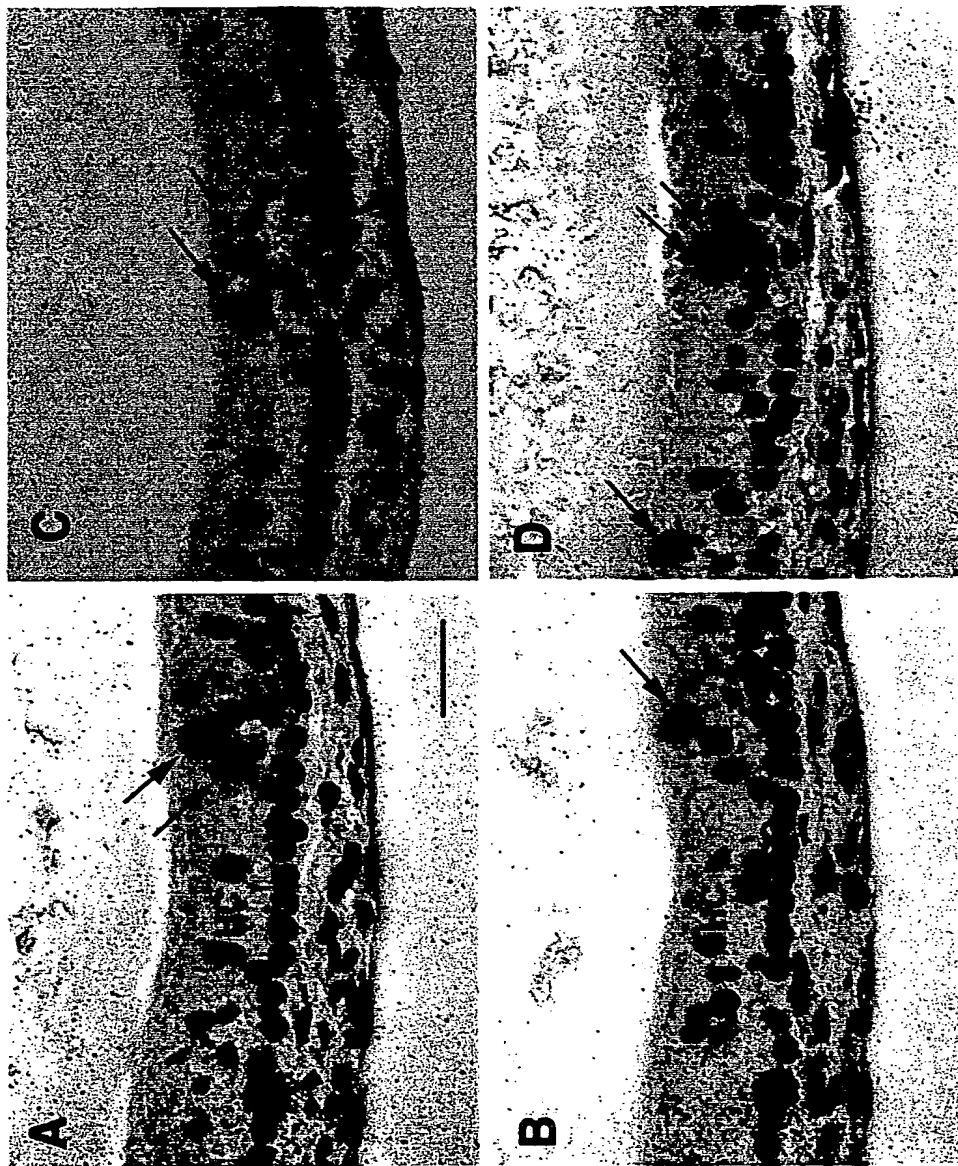


FIG.11

Heregulin Enhances the Numbers of ^3H -thymidine Labeled Cells in Both Supporting and Hair Cell Layers

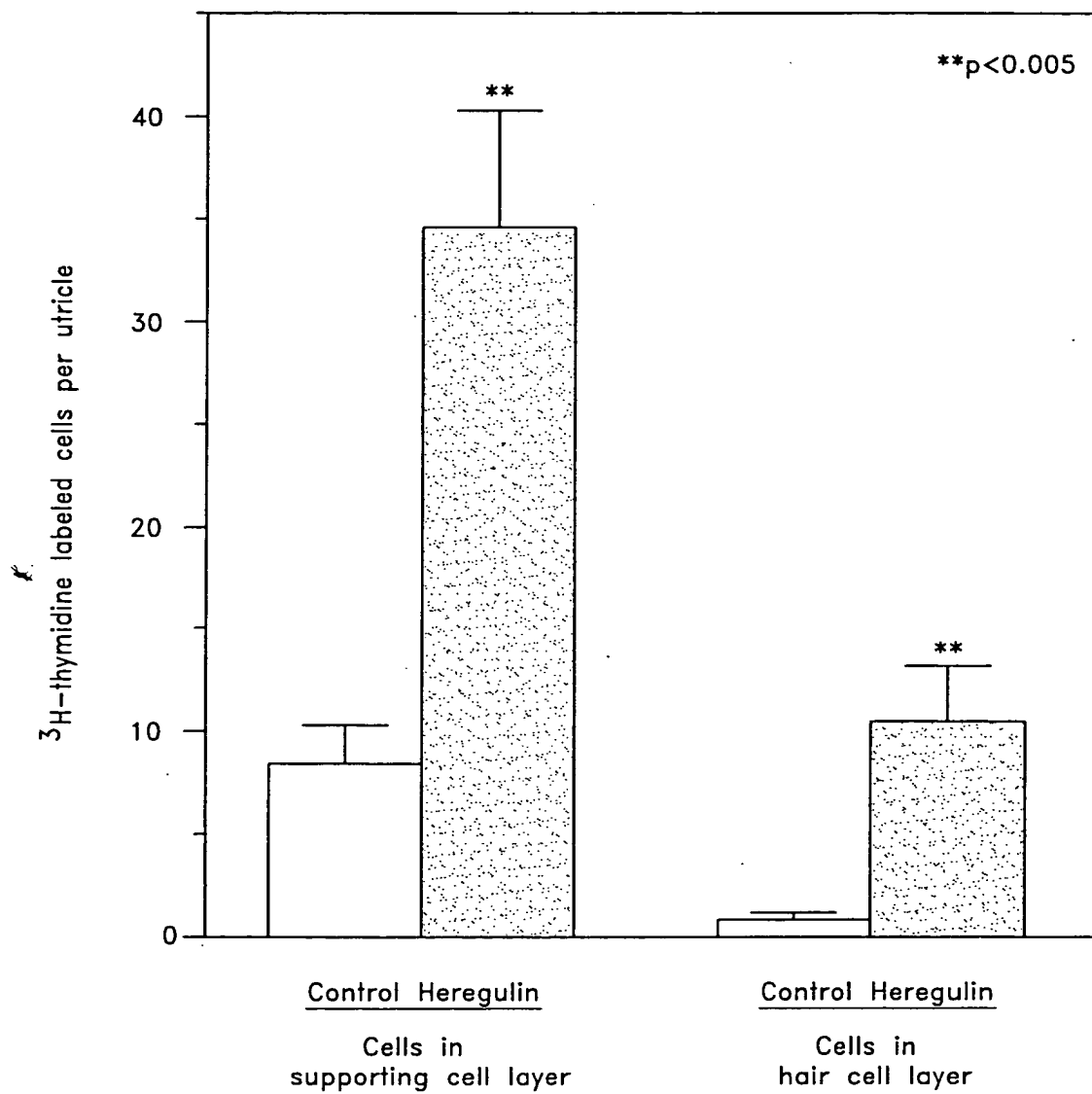
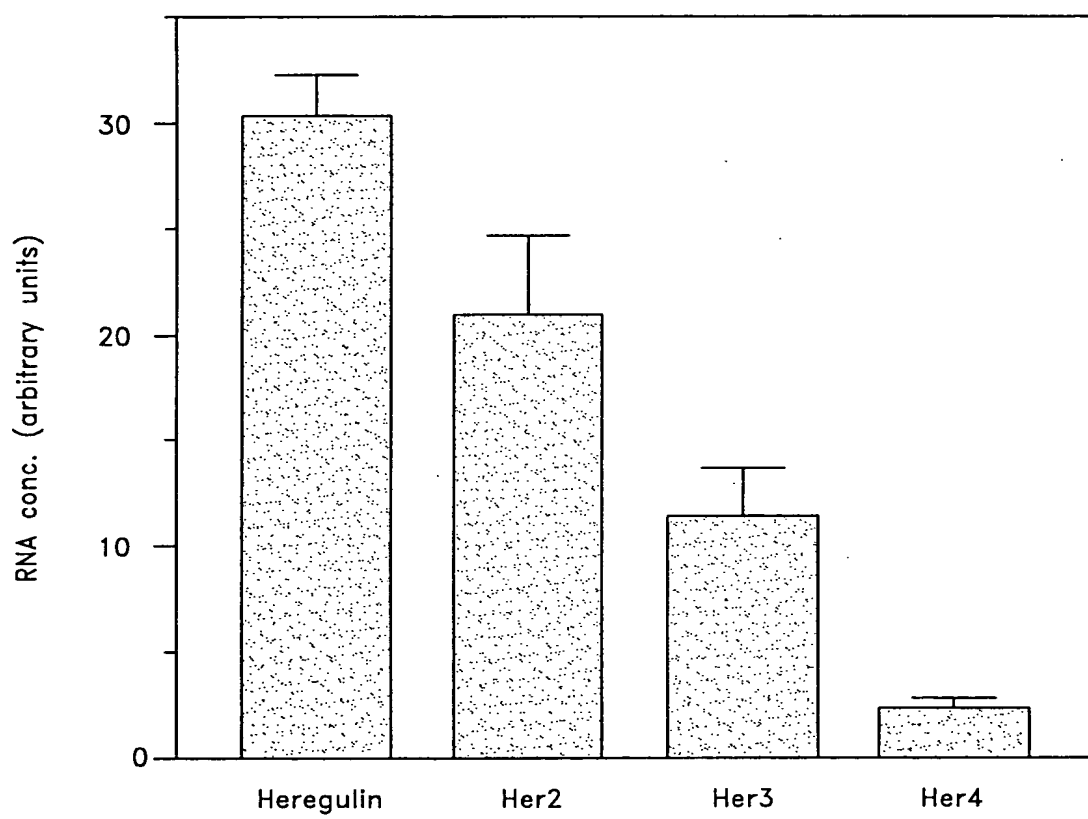


FIG. 12

*FIG. 13*

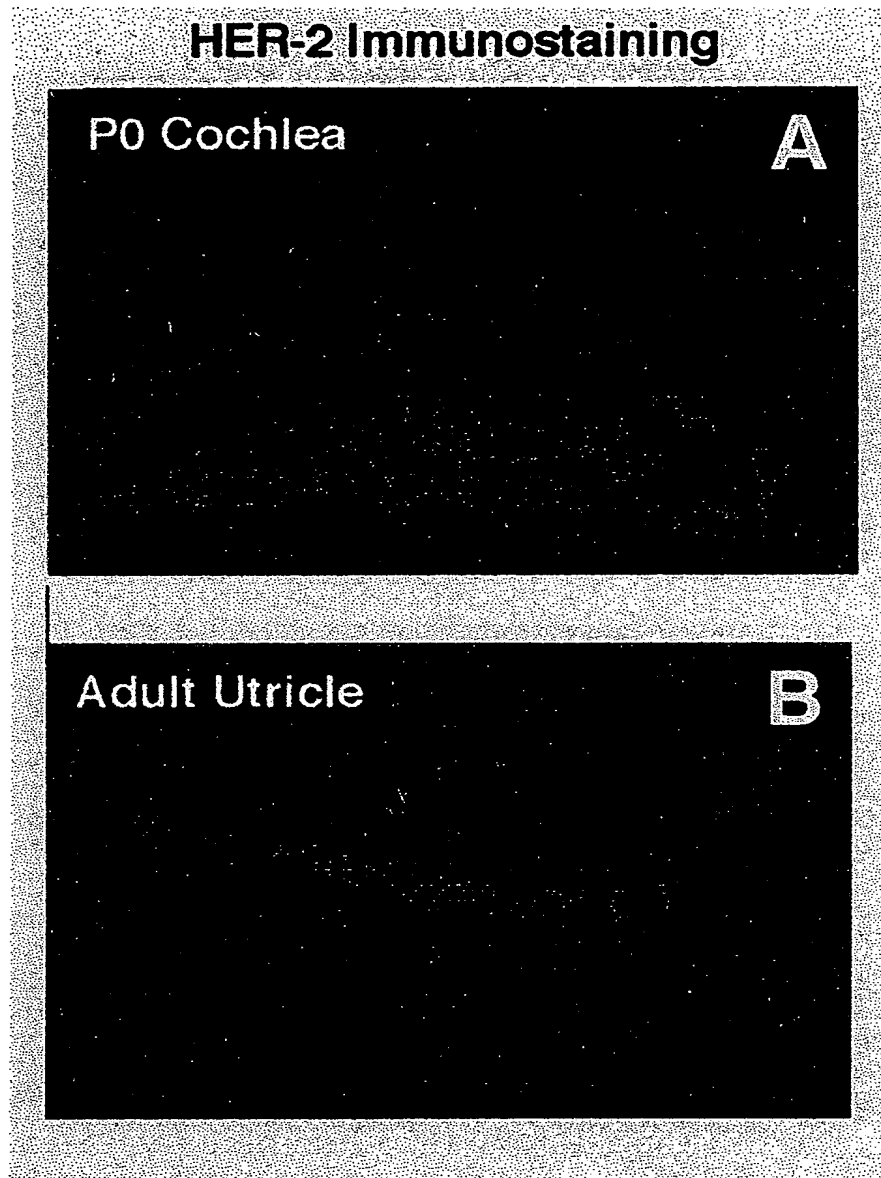


FIG.14